

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/994,365

DATE: 12/04/2001

TIME: 12:06:54

Input Set : A:\CECH18109seq.txt

Output Set: N:\CRF3\11212001\I994365.raw

ENTERED

3 <110> APPLICANT: Charmley, Patrick
4 Moss, Patrick
5 McEuen, Mark
7 <120> TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating
Psoriasis
9 <130> FILE REFERENCE: CECH118109
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/994,365
C--> 11 <141> CURRENT FILING DATE: 2001-11-26
11 <150> PRIOR APPLICATION NUMBER: US 60/253,592
12 <151> PRIOR FILING DATE: 2000-11-28
14 <150> PRIOR APPLICATION NUMBER: US 60/256,839
15 <151> PRIOR FILING DATE: 2000-12-15
17 <160> NUMBER OF SEQ ID NOS: 16
19 <170> SOFTWARE: PatentIn version 3.0
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22 <211> LENGTH: 891
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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27 <221> NAME/KEY: CDS
28 <222> LOCATION: (64)..(471)
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34 Met Ile Leu Asn Trp Lys Leu Leu Gly Ile Leu Val Leu Cys Leu
35 1 5 10 15
37 cac acc aga ggc atc tca ggc agc gag ggc cac ccc tct cac cca ccc 156
38 His Thr Arg Gly Ile Ser Gly Ser Glu Gly His Pro Ser His Pro Pro
39 20 25 30
41 gca gag gac cga gag gag gca ggc tcc cca aca ttg cct cag ggc ccc 204
42 Ala Glu Asp Arg Glu Glu Ala Gly Ser Pro Thr Leu Pro Gln Gly Pro
43 35 40 45
45 cca gtc ccc ggt gac cct tgg cca ggg gca ccc cct ctc ttt gaa gat 252
46 Pro Val Pro Gly Asp Pro Trp Pro Gly Ala Pro Pro Leu Phe Glu Asp
47 50 55 60
49 cct ccg cct acc cgc ccc agt cgt ccc tgg aga gac ctg cct gaa act 300
50 Pro Pro Pro Thr Arg Pro Ser Arg Pro Trp Arg Asp Leu Pro Glu Thr
51 65 70 75
53 gga gtc tgg ccc cct gaa ccg cct aga acg gat cct cct caa cct ccc 348
54 Gly Val Trp Pro Pro Glu Pro Pro Arg Thr Asp Pro Pro Gln Pro Pro
55 80 85 90 95
57 cgg cct gac gac cct tgg ccg gca gga ccc cag ccc cca gaa aac ccc 396
58 Arg Pro Asp Asp Pro Trp Pro Ala Gly Pro Gln Pro Pro Glu Asn Pro
59 100 105 110
61 tgg cct cct gcc cct gag gtg gac aac cga cct cag gag gag cca gac 444
62 Trp Pro Pro Ala Pro Glu Val Asp Asn Arg Pro Gln Glu Glu Pro Asp
63 115 120 125
65 cta gac cca ccc cgg gaa gag tac aga taatggagtc cctcagccg 491

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66 Leu Asp Pro Pro Arg Glu Glu Tyr Arg
67      130      135
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71 tcttcccaat ttagcctatc tccttaaacc tottctcat tccctcggtt ttattctgaa 611
73 cccgtaagggt ggtgttctca atatttctctg tccccctctg agatccatac ttagtctctca 671
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79 tactgtgttc ccttctgcca cctggtggcc ggcggcagga actatcagta gacagctgct 851
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85 <211> LENGTH: 136
86 <212> TYPE: PRT
87 <213> ORGANISM: Homo sapiens
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95 Thr Arg Gly Ile Ser Gly Ser Glu Gly His Pro Ser His Pro Pro Ala
96      20      25      30
99 Glu Asp Arg Glu Glu Ala Gly Ser Pro Thr Leu Pro Gln Gly Pro Pro
100      35      40      45
103 Val Pro Gly Asp Pro Trp Pro Gly Ala Pro Pro Leu Phe Glu Asp Pro
104      50      55      60
107 Pro Pro Thr Arg Pro Ser Arg Pro Trp Arg Asp Leu Pro Glu Thr Gly
108 65      70      75      80
111 Val Trp Pro Pro Glu Pro Pro Arg Thr Asp Pro Pro Gln Pro Pro Arg
112      85      90      95
115 Pro Asp Asp Pro Trp Pro Ala Gly Pro Gln Pro Pro Glu Asn Pro Trp
116      100      105      110
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123 Asp Pro Pro Arg Glu Glu Tyr Arg
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128 <211> LENGTH: 114
129 <212> TYPE: PRT
130 <213> ORGANISM: Homo sapiens
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138      20      25      30
140 Pro Gly Ala Pro Pro Leu Phe Glu Asp Pro Pro Pro Thr Arg Pro Ser
141      35      40      45
143 Arg Pro Trp Arg Asp Leu Pro Glu Thr Gly Val Trp Pro Pro Glu Pro
144      50      55      60
146 Pro Arg Thr Asp Pro Gln Pro Pro Arg Pro Asp Asp Pro Trp Pro
147 65      70      75      80
149 Ala Gly Pro Gln Pro Pro Glu Asn Pro Trp Pro Pro Ala Pro Glu Val
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168 cccgcttcgg cctcccaaag tgctgggatt acaggcgcaa gccaccacac caggcccgcg      180
170 tgatgtatat tttaagacct cttttgctgg tggaggacag gctttgtgtg agggggaggg      240
172 ataaacagtg ggagcaaggg ggccaattag aagggtgttg gggaggctca ggggagatgg      300
174 tggtcaggga tgatgggctg ggtttggaca ggggtgtggag gggcttgca ggtgatggtg      360
176 gaggagtgtg acgaagggtt ctgctgagc cctggaggga acagatgaga tcacgccatt      420
178 gcataataag gtgttcttta ctgtggggtg gcggaaccag cagggaacaa cctgggagga      480
180 atcaaatttt attttggaca tgttacttct gaaaggctaa cagacttcca ggcagaaagg      540
182 tccttgaggg aaacgttcta ggggtctctc tgggaggctt agatcaagga gctgagacca      600
184 aaaggagaat gggaggagg agacgagtac aatagagttg gagccaaggc cctagaggcg      660
186 gataggtgga ttctgaggg aggaggaagg ggctgaggtt gctggagcct ggcagcttct      720
188 tccggagcca ttggcaggac tgatgcaaac agctctgggt gggagagggg aaccaggata      780
190 tcctcctgtg tccttctctt tctgcagtca tcctgggtgg ctgccagatg gaattccttg      840
192 gatatacattg cttggagggt ccctgcatgc ctgaagaagg acatggtgga gagcaggatg      900
194 cctggatccc atgggggaag ggaagtgcgc aggaagcac gaagccccag ggggagcttt      960
196 cagtgcgggg atgagtgggg aggctggggg agtagctgac actgtcccag ctgcatccca      1020
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200 gtgcttccca acgcccacg cgtggtttgc tccattctt tggcttcaa tagttgcaag      1140
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222 tttgctggct ccatgtggca aagtcgggtc ggattaacgt ggggggggac gagtttctc      1800
224 ggagctggga tctgtgttaa ggagctgggt tccttgtaaa gctgggtct gtgtgctgg      1860
226 gggccaagggt gtaaccacc ttgggttgca ggttggcctg aggacaaagc tagtggggta      1920
228 ccccaaccag ggggtgatgg agcttatttg gagaagtctg gtcagtttaa agtgggtcaa      1980
230 gtgaacggtt cagatccatc gggggtaggg gttcatgaca ttttaccatc agttaagtat      2040
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234 aggtgcgtc catccagaca ggctcctcct cctggggctg gggctgggtg gggctgggga      2160
236 gagaagccct caccacctt tacctttctc ctctcctctt tacaggcatc tcaggcagcg      2220
238 agggccaccc ctctcaccca ccgcagagg accgagagga ggcaggctcc ccaacattgc      2280
240 ctcagggccc ccagtcctcc ggtgacctt ggccaggggc acccctctc tttgaagatc      2340
242 ctccgcctac ccgcccagc cgtccctgga gagacctgcc tgaactgga gtctggcccc      2400
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250 ctgttcccag gcatctccag gcaccacgc cctctccacc ctctgattcc ccgtgaattc 2640
252 ttcccaattht agcctatctc cttaaacttc ttctctattc cctcggtttt attctgaacc 2700
254 cgtaagggtg tggttctcaat atttctgtc ccctcctgag atccatactt agtcctcaca 2760
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258 cccacactac ctcccaccg gtcttctctgc ccgcgcgac gctggggcag ggctatggta 2880
260 ctgtgttccc ttctgccacc tgggtggcgg cggcaggaac tatcagtaga cagctgctgc 2940
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279 1 5 10 15
281 gtc tgt ctt cat ctc cca ggc ctc ttt gcc cgg agc atc ggt gtt gtg 96
282 Val Cys Leu His Leu Pro Gly Leu Phe Ala Arg Ser Ile Gly Val Val
283 20 25 30
285 gag gag aaa gtt tcc caa aac ttg ggg acc aac ttg cct cag ctc gga 144
286 Glu Glu Lys Val Ser Gln Asn Leu Gly Thr Asn Leu Pro Gln Leu Gly
287 35 40 45
289 caa cct tcc tcc act ggc ccc tct aac tct gaa cat ccg cag ccc gct 192
290 Gln Pro Ser Ser Thr Gly Pro Ser Asn Ser Glu His Pro Gln Pro Ala
291 50 55 60
293 ctg gac cct agg tct aat gac ttg gca agg gtt cct ctg aag ctc agc 240
294 Leu Asp Pro Arg Ser Asn Asp Leu Ala Arg Val Pro Leu Lys Leu Ser
295 65 70 75 80
297 gtg cct gca tca gat ggc ttc cca cct gca gga ggt tct gca gtg cag 288
298 Val Pro Ala Ser Asp Gly Phe Pro Pro Ala Gly Gly Ser Ala Val Gln
299 85 90 95
301 agg tgg cct cca tcg tgg ggg ctg cct gcc atg gat tcc tgg ccc cct 336
302 Arg Trp Pro Pro Ser Trp Gly Leu Pro Ala Met Asp Ser Trp Pro Pro
303 100 105 110
305 gag gat cct tgg cag atg atg gct gct gcg gct gag gac cgc ctg ggg 384
306 Glu Asp Pro Trp Gln Met Met Ala Ala Ala Ala Glu Asp Arg Leu Gly
307 115 120 125
309 gaa gcg ctg cct gaa gaa ctc tct tac ctc tcc agt gct gcg gcc ctc 432
310 Glu Ala Leu Pro Glu Glu Leu Ser Tyr Leu Ser Ser Ala Ala Ala Leu
311 130 135 140
313 gct ccg ggc agt ggc cct ttg cct ggg gag tct tct ccc gat gcc aca 480
314 Ala Pro Gly Ser Gly Pro Leu Pro Gly Glu Ser Ser Pro Asp Ala Thr
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317 ggc ctc tca ccc gag gct tca ctc ctc cac cag gac tcg gag tcc aga 528

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322 Arg Leu Pro Arg Ser Asn Ser Leu Gly Ala Gly Gly Lys Ile Leu Ser
323          180          185          190
325 caa cgc cct ccc tgg tct ctc atc cac agg gtt ctg cct gat cac ccc      624
326 Gln Arg Pro Pro Trp Ser Leu Ile His Arg Val Leu Pro Asp His Pro
327          195          200          205
329 tgg ggt acc ctg aat ccc agt gtg tcc tgg gga ggt gga ggc cct ggg      672
330 Trp Gly Thr Leu Asn Pro Ser Val Ser Trp Gly Gly Gly Gly Pro Gly
331          210          215          220
333 act ggt tgg gga acg agg ccc atg cca cac cct gag gga atc tgg ggt      720
334 Thr Gly Trp Gly Thr Arg Pro Met Pro His Pro Glu Gly Ile Trp Gly
335 225          230          235          240
337 atc aat aat caa ccc cca ggt acc agc tgg gga aat att aat cgg tat      768
338 Ile Asn Asn Gln Pro Pro Gly Thr Ser Trp Gly Asn Ile Asn Arg Tyr
339          245          250          255
341 cca gga ggc agc tgg gga aat att aat cgg tat cca gga ggc agc tgg      816
342 Pro Gly Gly Ser Trp Gly Asn Ile Asn Arg Tyr Pro Gly Gly Ser Trp
343          260          265          270
345 ggg aat att aat cgg tat cca gga ggc agc tgg ggg aat att cat cta      864
346 Gly Asn Ile Asn Arg Tyr Pro Gly Gly Ser Trp Gly Asn Ile His Leu
347          275          280          285
349 tac cca ggt atc aat aac cca ttt cct cct gga gtt ctc cgc cct cct      912
350 Tyr Pro Gly Ile Asn Asn Pro Phe Pro Pro Gly Val Leu Arg Pro Pro
351          290          295          300
353 ggc tct tct tgg aac atc cca gct ggc ttc cct aat cct cca agc cct      960
354 Gly Ser Ser Trp Asn Ile Pro Ala Gly Phe Pro Asn Pro Pro Ser Pro
355 305          310          315          320
357 agg ttg cag tgg ggc tag agcacgatag agggaaaccc aacattggga      1008
358 Arg Leu Gln Trp Gly
359          325
361 gttagagtcc tgctccgcgc ccttgctgtg tgggctcaat ccaggccctg ttaacatggt      1068
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380          20          25          30
383 Glu Glu Lys Val Ser Gln Asn Leu Gly Thr Asn Leu Pro Gln Leu Gly
384          35          40          45
387 Gln Pro Ser Ser Thr Gly Pro Ser Asn Ser Glu His Pro Gln Pro Ala
388          50          55          60
391 Leu Asp Pro Arg Ser Asn Asp Leu Ala Arg Val Pro Leu Lys Leu Ser

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date